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 NEWS  1           Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2           "Ask CAS" for self-help around the clock
 NEWS  3  SEP 09   CA/CAplus records now contain indexing from 1907 to the
                   present
 NEWS  4  DEC 08   INPADOC: Legal Status data reloaded
 NEWS  5  SEP 29   DISSABS now available on STN
 NEWS  6  OCT 10   PCTFULL: Two new display fields added
 NEWS  7  OCT 21   BIOSIS file reloaded and enhanced
 NEWS  8  OCT 28   BIOSIS file segment of TOXCENTER reloaded and enhanced
 NEWS  9  NOV 24   MSDS-CCOHS file reloaded
 NEWS 10  DEC 08   CABA reloaded with left truncation
 NEWS 11  DEC 08   IMS file names changed
 NEWS 12  DEC 09   Experimental property data collected by CAS now available
                   in REGISTRY
 NEWS 13  DEC 09   STN Entry Date available for display in REGISTRY and CA/CAplus
 NEWS 14  DEC 17   DGENE: Two new display fields added
 NEWS 15  DEC 18   BIOTECHNO no longer updated
 NEWS 16  DEC 19   CROPU no longer updated; subscriber discount no longer
                   available
 NEWS 17  DEC 22   Additional INPI reactions and pre-1907 documents added to CAS
                   databases
 NEWS 18  DEC 22   IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
 NEWS 19  DEC 22   ABI-INFORM now available on STN
 NEWS 20  JAN 27   Source of Registration (SR) information in REGISTRY updated
                   and searchable
 NEWS 21  JAN 27   A new search aid, the Company Name Thesaurus, available in
                   CA/CAplus
 NEWS 22  FEB 05   German (DE) application and patent publication number format
                   changes

 NEWS EXPRESS  DECEMBER 28 CURRENT WINDOWS VERSION IS V7.00, CURRENT
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FILE 'HOME' ENTERED AT 17:37:06 ON 10 FEB 2004

=> file medline, biosis, uspatful, dgene, embase, wpids, fsta, japio, jicst
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       0.21       0.21

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=> s gene () reiterated
L1            6 GENE (W) REITERATED

=> s ribosomal DNA
L2        19510 RIBOSOMAL DNA

=> d l1 ti abs ibib tot

L1   ANSWER 1 OF 6     MEDLINE on STN
TI   Wpkci, encoding an altered form of PKCI, is conserved widely on the avian
     W chromosome and expressed in early female embryos: implication of its
     role in female sex determination.
AB   Two W chromosome-linked cDNA clones, p5fm2 and p5fm3, were obtained from a
     subtracted (female minus male) cDNA library prepared from a mixture of
     undifferentiated gonads and mesonephroi of male or female 5-d (stages
     26-28) chicken embryos.  These two clones were demonstrated to be derived
     from the mRNA encoding an altered form of PKC inhibitor/interacting
     protein (PKCI), and its gene was named Wpkci.  The Wpkci gene
     reiterated approximately 40 times tandemly and located at the
     nonheterochromatic end of the chicken W chromosome.  The W linkage and the
     moderate reiteration of Wpkci were conserved widely in Carinatae birds.
     The chicken PKCI gene, chPKCI, was shown to be a single-copy gene located
     near the centromere on the long arm of the Z chromosome.  Deduced amino
     acid sequences of Wpkci and chPKCI showed approximately 65% identity.  In
     the deduced sequence of Wpkci, the HIT motif, which is essential for PKCI
     function, was absent, but the alpha-helix region, which was conserved
     among the PKCI family, and a unique Leu- and Arg-rich region, were
     present.  Transcripts from both Wpkci and chPKCI genes were present at
     significantly higher levels in 3- to 6-d (stages 20-29) embryos.  These
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transcripts were detected in several embryonic tissues, including undifferentiated left and right gonads. When the green fluorescent protein-fused form of Wpkci was expressed in male chicken embryonic fibroblast, it was located almost exclusively in the nucleus. A model is presented suggesting that Wpkci may be involved in triggering the differentiation of ovary by interfering with PKCI function or by exhibiting its unique function in the nuclei of early female embryos.

ACCESSION NUMBER: 2001040272 MEDLINE
DOCUMENT NUMBER: 20483789 PubMed ID: 11029061
TITLE: Wpkci, encoding an altered form of PKCI, is conserved widely on the avian W chromosome and expressed in early female embryos: implication of its role in female sex determination.
AUTHOR: Hori T; Asakawa S; Itoh Y; Shimizu N; Mizuno S
CORPORATE SOURCE: Laboratory of Molecular Biology, Department of Molecular and Cell Biology, Graduate School of Agricultural Science, Tohoku University, Sendai 981-8555 Japan.
SOURCE: MOLECULAR BIOLOGY OF THE CELL, (2000 Oct) 11 (10) 3645-60. Journal code: 9201390. ISSN: 1059-1524.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200012
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001207

L1 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI Wpkci, encoding an altered form of PKCI, is conserved widely on the avian W chromosome and expressed in early female embryos: Implication of its role in female sex determination.
AB Two W chromosome-linked cDNA clones, p5fm2 and p5fm3, were obtained from a subtracted (female minus male) cDNA library prepared from a mixture of undifferentiated gonads and mesonephroi of male or female 5-d (stages 26-28) chicken embryos. These two clones were demonstrated to be derived from the mRNA encoding an altered form of PKC inhibitor/interacting protein (PKCI), and its gene was named Wpkci. The Wpkci **gene reiterated** apprx40 times tandemly and located at the nonheterochromatic end of the chicken W chromosome. The W linkage and the moderate reiteration of Wpkci were conserved widely in Carinatae birds. The chicken PKCI gene, chPKCI, was shown to be a single-copy gene located near the centromere on the long arm of the Z chromosome. Deduced amino acid sequences of Wpkci and chPKCI showed apprx65% identity. In the deduced sequence of Wpkci, the HIT motif, which is essential for PKCI function, was absent, but the alpha-helix region, which was conserved among the PKCI family, and a unique Leu- and Arg-rich region, were present. Transcripts from both Wpkci and chPKCI genes were present at significantly higher levels in 3- to 6-d (stages 20-29) embryos. These transcripts were detected in several embryonic tissues, including undifferentiated left and right gonads. When the green fluorescent protein-fused form of Wpkci was expressed in male chicken embryonic fibroblast, it was located almost exclusively in the nucleus. A model is presented suggesting that Wpkci may be involved in triggering the differentiation of ovary by interfering with PKCI function or by exhibiting its unique function in the nuclei of early female embryos.
ACCESSION NUMBER: 2001:127785 BIOSIS
DOCUMENT NUMBER: PREV200100127785
TITLE: Wpkci, encoding an altered form of PKCI, is conserved widely on the avian W chromosome and expressed in early female embryos: Implication of its role in female sex determination.
AUTHOR(S): Hori, Tetsuya; Asakawa, Shuichi; Itoh, Yuichiro; Shimizu, Nobuyoshi; Mizuno, Shigeki [Reprint author]

CORPORATE SOURCE: Laboratory of Molecular Biology, Department of Molecular and Cell Biology, Graduate School of Agricultural Science, Tohoku University, Sendai, 981-8555, Japan
s-mizuno@brs.nihon-u.ac.jp
SOURCE: Molecular Biology of the Cell, (October, 2000) Vol. 11, No. 10, pp. 3645-3660. print.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Article
LANGUAGE: English
OTHER SOURCE: Genbank-AB026675; EMBL-AB026675; DDBJ-AB026675; Genbank-AB026677; EMBL-AB026677; DDBJ-AB026677
ENTRY DATE: Entered STN: 14 Mar 2001
Last Updated on STN: 18 Feb 2002

L1 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI Reiterated repeat region variability in the ciliary adhesin gene of Mycoplasm hyopneumoniae.
AB Mycoplasma hyopneumoniae is a highly prevalent pathogen which colonizes the ciliated epithelial lining of the porcine respiratory tract. Expression libraries constructed from genomic DNA of the non-pathogenic strain M. hyopneumoniae J were screened with porcine hyperimmune antiserum against M. hyopneumoniae. One clone expressed a 28 kDa protein which was also reactive with monospecific antiserum raised against a putative M. hyopneumoniae-specific 94 kDa antigen derived from strain J. Trypsin digestion of whole M. hyopneumoniae cells showed the 94 kDa antigen to be surface-accessible. DNA sequence analysis of the gene encoding the 94 kDa antigen revealed greater than 90% homology to two adhesin genes, encoding P97 and Mhp1, cloned from pathogenic strain 232 and strain P5722 of M. hyopneumoniae, respectively. Two regions of repetitive DNA sequence were identified in the gene encoding the 94 kDa antigen. The first encoded the deduced amino acid sequence A(T)-K-P-E(V)-A(T) arranged as nine tandem repeats (RR1). The second region of repetitive DNA sequence encoded the deduced amino acid sequence G-A(E,S)-P-N(S)-Q-G-K-K-A-E arranged as five tandem repeats (RR2). Comparison of the three M. hyopneumoniae adhesin genes revealed that the genes encoding P97 and Mhp1, and the strain J gene encoding the 94 kDa antigen contained 15, 12 and 9 tandem repeats, respectively, in RR1, and 4, 5 and 5 tandem repeats, respectively, in RR2. Southern hybridization analysis of EcoRI-digested genomic DNA probed with an 820 bp fragment spanning RR1 and RR2 identified a strongly hybridizing fragment ranging in size from 2.15 to 2.30 kb among seven geographically diverse strains of M. hyopneumoniae but failed to hybridize with DNA from four strains of Mycoplasma hyorhinis or Mycoplasma flocculare strain Ms42. PCR primers flanking the DNA sequence encoding RR1 and RR2 were used to amplify DNA from the seven strains of M. hyopneumoniae and DNA sequence analysis of the amplification products showed that the number of tandem amino acid repeats in RR1 varied considerably between strains. RR1 from M. hyopneumoniae strains YZ, Beaufort, Sue, OMZ407 and C1735/2 comprised 11, 15, 12, 15 and 8 tandem copies, respectively, of the 5-aa repeat whilst RR2 comprised 4, 3, 4, 3 and 4 tandem copies, respectively, of the 10-aa repeat. Two putative integrin binding sites (L-E-T and R-X-X-X-D) were identified in the 94 kDa ciliary adhesin. Variability in the number of amino acid repeats in RR1 amongst strains of M. hyopneumoniae may influence ciliary binding.
ACCESSION NUMBER: 1998:391142 BIOSIS
DOCUMENT NUMBER: PREV199800391142
TITLE: Reiterated repeat region variability in the ciliary adhesin gene of Mycoplasm hyopneumoniae.
AUTHOR(S): Wilton, Jody L.; Scarman, Anthony L.; Walker, Mark J.; Djordjevic, Steven P. [Reprint author]
CORPORATE SOURCE: Microbiol. and Immunol. Sect., Elizabeth Macarthur Agric. Inst., PMB 8, Camden, NSW 2570, Australia
SOURCE: Microbiology (Reading), (July, 1998) Vol. 144, No. 7, pp. 1931-1943. print.
ISSN: 1350-0872.

DOCUMENT TYPE: Article
LANGUAGE: English
OTHER SOURCE: Genbank-AF001398
ENTRY DATE: Entered STN: 10 Sep 1998
Last Updated on STN: 10 Sep 1998

L1 ANSWER 4 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI VARIABILITY OF THE REGION OF THE HERPES SIMPLEX VIRUS TYPE 1 GENOME YIELDING DEFECTIVE DNA S M A-I FRAGMENT POLYMORPHISM.
AB A SmaI map of class I defective DNA of herpes simplex virus type 1 (HSVI) was constructed using a set of deletion hybrid phages. Four SmaI fragments on the defective DNA had a variability in length common among 15 HSVI isolates: the 1.45 kilobase (kb) fragment located within the BamHI-Z (map coordinates 0.936-0.949) fragment, the 0.92-kb fragment neighboring on the a sequence, the 0.44-kb fragment containing the intervening sequence of immediate-early mRNA-5 gene, and the 0.205-kb fragment corresponding to the a sequence. The 4 SmaI fragments have several sets of reiterated sequences, among which the 1.45- and 0.92-kb fragments hybridized with mammalian cellular DNA (human, monkey, rabbit and mouse).
ACCESSION NUMBER: 1985:351746 BIOSIS
DOCUMENT NUMBER: PREV198580021738; BA80:21738
TITLE: VARIABILITY OF THE REGION OF THE HERPES SIMPLEX VIRUS TYPE 1 GENOME YIELDING DEFECTIVE DNA S M A-I FRAGMENT POLYMORPHISM.
AUTHOR(S): UMENE K [Reprint author]
CORPORATE SOURCE: DEP OF VIROLOGY, FACULTY OF MEDICINE, KYUSHU UNIVERSITY 60, FUKUOKA, 812 JAPAN
SOURCE: Intervirology, (1985) Vol. 23, No. 3, pp. 131-139.
CODEN: IVRYAK. ISSN: 0300-5526.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH

L1 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI QUANTITATIVE REGULATION OF TRANSCRIPTION IN EUKARYOTES THEORETICAL CONSIDERATIONS OF RNA POLYMERASE INVOLVEMENT.
AB Possible points of regulation in the transcription cycles of the 3 major classes of eukaryotic genes are considered on a theoretical basis in the light of recent information on gene and RNA polymerase numbers. The 3 types of coding sequences are controlled in different ways. Class I cistrons (nucleolar ribosomal genes) would seem most amenable to quantitative regulation by alteration of polymerase elongation rates or of the numbers of these (reiterated) sequences available to the enzyme. Class II genes (structural, protein-coding) are more likely to be controlled at the point of initiation of RNA synthesis. Class III genes (small ribosomal and transfer RNA coding sequences) are probably mainly controlled by altering the numbers of (reiterated) cistrons available to the polymerase. Relevant experimental observations are also discussed.
ACCESSION NUMBER: 1981:175168 BIOSIS
DOCUMENT NUMBER: PREV198171045160; BA71:45160
TITLE: QUANTITATIVE REGULATION OF TRANSCRIPTION IN EUKARYOTES THEORETICAL CONSIDERATIONS OF RNA POLYMERASE INVOLVEMENT.
AUTHOR(S): BEEBEE T J C [Reprint author]
CORPORATE SOURCE: DEP BIOCHEM, UNIV SUSSEX, FALMER, BRIGHTON BN1 9QG, SUSSEX, ENGLAND, UK
SOURCE: Journal of Theoretical Biology, (1980) Vol. 86, No. 4, pp. 803-815.
CODEN: JTBIAP. ISSN: 0022-5193.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH

L1 ANSWER 6 OF 6 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

TI Wpkci, encoding an altered form of PKCI, is conserved widely on the avian W chromosome and expressed in early female embryos: Implication of its role in female sex determination.

AB Two W chromosome-linked cDNA clones, p5fm2 and p5fm3, were obtained from a subtracted (female minus male) cDNA library prepared from a mixture of undifferentiated gonads and mesonephroi of male or female 5-d (stages 26-28) chicken embryos. These two clones were demonstrated to be derived from the mRNA encoding an altered form of PKC inhibitor/interacting protein (PKCI), and its gene was named Wpkci. The Wpkci **gene reiterated** .apprx.40 times tandemly and located at the nonheterochromatic end of the chicken W chromosome. The W linkage and the moderate reiteration of Wpkci were conserved widely in Carinatae birds. The chicken PKCI gene, chPKCI, was shown to be a single-copy gene located near the centromere on the long arm of the Z chromosome. Deduced amino acid sequences of Wpkci and chPKCI showed .apprx.65% identity. In the deduced sequence of Wpkci, the HIT motif, which is essential for PKCI function, was absent, but the α-helix region, which was conserved among the PKCI family, and a unique Leu- and Arg-rich region, were present. Transcripts from both Wpkci and chPKCI genes were present at significantly higher levels in 3- to 6-d (stages 20-29) embryos. These transcripts were detected in several embryonic tissues, including undifferentiated left and right gonads. When the green fluorescent protein-fused form of Wpkci was expressed in male chicken embryonic fibroblast, it was located almost exclusively in the nucleus. A model is presented suggesting that Wpkci may be involved in triggering the differentiation of ovary by interfering with PKCI function or by exhibiting its unique function in the nuclei of early female embryos.

ACCESSION NUMBER: 2000371531 EMBASE
TITLE: Wpkci, encoding an altered form of PKCI, is conserved widely on the avian W chromosome and expressed in early female embryos: Implication of its role in female sex determination.
AUTHOR: Hori T.; Asakawa S.; Itoh Y.; Shimizu N.; Mizuno S.
CORPORATE SOURCE: S. Mizuno, Dept. of Molecular and Cell Biology, Graduate Sch. of Agricultural Sci., Tohoku University, Sendai 981-8555, Japan. s-mizuno@brs.nihon-u.ac.jp
SOURCE: Molecular Biology of the Cell, (2000) 11/10 (3645-3660). Refs: 41
ISSN: 1059-1524 CODEN: MBCEEV
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 021 Developmental Biology and Teratology
022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English

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=> d his

     (FILE 'HOME' ENTERED AT 17:37:06 ON 10 FEB 2004)

     FILE 'MEDLINE, BIOSIS, USPATFULL, DGENE, EMBASE, WPIDS, FSTA, JAPIO,
     JICST-EPLUS' ENTERED AT 17:37:27 ON 10 FEB 2004
L1             6 S GENE () REITERATED
L2         19510 S RIBOSOMAL DNA

=> s l1 and l1
L3             6 L1 AND L1

=> s l1 and l2
L4             0 L1 AND L2

=> s reiterated ribosomal DNA
L5            13 REITERATED RIBOSOMAL DNA
```

=> s gene integrated
L6 1278 GENE INTEGRATED

=> d l5 ti abs ibib tot

L5 ANSWER 1 OF 13 MEDLINE on STN
TI Recombination and mutagenesis in rad6 mutants of Saccharomyces cerevisiae: evidence for multiple functions of the RAD6 gene.
AB The rad6-1 and rad6-3 mutants are highly UV sensitive and show an increase in spontaneous and UV induced mitotic heteroallelic recombination in diploids. Both rad6 mutants are proficient in spontaneous and UV induced unequal sister chromatid recombination in the **reiterated ribosomal DNA** sequence and are deficient in UV induced mutagenesis. In contrast to the above effects where both mutants appear similar, rad6-1 mutants are deficient in sporulation and meiotic recombination whereas rad6-3 mutants are proficient. The differential effects of these mutations indicate that the RAD6 gene is multifunctional. The possible role of the RAD6 gene in error prone excision repair of UV damage during the G1 phase of the cell cycle in addition to its role in postreplication repair is discussed.
ACCESSION NUMBER: 82147786 MEDLINE
DOCUMENT NUMBER: 82147786 PubMed ID: 7038392
TITLE: Recombination and mutagenesis in rad6 mutants of Saccharomyces cerevisiae: evidence for multiple functions of the RAD6 gene.
AUTHOR: Montelone B A; Prakash S; Prakash L
CONTRACT NUMBER: GM19261 (NIGMS)
SOURCE: MOLECULAR AND GENERAL GENETICS, (1981) 184 (3) 410-5. Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY, WEST: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198205
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 19970203
Entered Medline: 19820527

L5 ANSWER 2 OF 13 MEDLINE on STN
TI Divergence of primate ribosomal RNA genes as assayed by restriction enzyme analysis.
AB Primate ribosomal RNA (rRNA) genes have been compared by restriction endonuclease mapping. In all species examined, the restriction map of the **reiterated ribosomal DNA** is simple (within the limits of detection by hybridization with rRNA) and is consistent with a high degree of homogeneity among the repeats. Within a species, all members have similar rDNA restriction patterns. However, different species of primates have distinctly different rDNA restriction maps; even chimpanzee and man can be discerned by their rDNA restriction patterns. Possible mechanisms for maintenance of homogeneity of the rDNA repeats within a species, while allowing divergence among closely related species, are discussed.
ACCESSION NUMBER: 81067916 MEDLINE
DOCUMENT NUMBER: 81067916 PubMed ID: 6254856
TITLE: Divergence of primate ribosomal RNA genes as assayed by restriction enzyme analysis.
AUTHOR: Nelkin B; Strayer D; Vogelstein B
CONTRACT NUMBER: CA 06973 (NCI)
SOURCE: GENE, (1980 Oct) 11 (1-2) 89-96. Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
ENTRY MONTH: 198102
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19980206
Entered Medline: 19810226

L5 ANSWER 3 OF 13 MEDLINE on STN
TI Simple Mendelian inheritance of the **reiterated ribosomal DNA** of yeast.
AB A diploid strain of yeast (Saccharomyces cerevisiae) was found to be heterozygous for two forms of the highly repetitious ribosomal DNA. These forms could be distinguished by the pattern of fragments produced after digestion with the site-specific restriction endonuclease EcoRI. The mode of inheritance of ribosomal DNA was determined by tetrad analysis. Of 14 tetrads analyzed, 12 clearly showed the ribosomal DNA forms segregating as a single Mendelian unit. The simplest interpretation of this result is that all of the approximately 100 copies of the ribosomal DNA genes of the yeast cell are located on one chromosome and that meiotic recombination within these genes is suppressed. Two of the 14 tetrads showed the segregation patterns expected as the result of mitotic recombination within the ribosomal DNA.
ACCESSION NUMBER: 78053057 MEDLINE
DOCUMENT NUMBER: 78053057 PubMed ID: 337310
TITLE: Simple Mendelian inheritance of the **reiterated ribosomal DNA** of yeast.
AUTHOR: Petes T D; Botstein D
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1977 Nov) 74 (11) 5091-5.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 197801
ENTRY DATE: Entered STN: 19900314
Last Updated on STN: 19900314
Entered Medline: 19780127

L5 ANSWER 4 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI RECOMBINATION AND MUTAGENESIS IN RAD-6 MUTANTS OF SACCHAROMYCES-CEREVISIAE EVIDENCE FOR MULTIPLE FUNCTIONS OF THE RAD-6 GENE.
AB The rad6-1 and rad6-3 mutants are highly UV sensitive and show an increase in spontaneous and UV induced mitotic heteroallelic recombination in diploids. Both rad6 mutants are proficient in spontaneous and UV induced unequal sister chromatid recombination in the **reiterated ribosomal DNA** sequence and are deficient in UV induced mutagenesis. In contrast to the above effects where both mutants appear similar, rad6-1 mutants are deficient in sporulation and meiotic recombination whereas rad6-3 mutants are proficient. The differential effects of these mutations indicate that the RAD6 gene is multifunctional. The possible role of the RAD6 gene in error prone excision repair of UV damage during the G1 phase of the cell cycle in addition to its role in postreplication repair is discussed.
ACCESSION NUMBER: 1982:237492 BIOSIS
DOCUMENT NUMBER: PREV198274009972; BA74:9972
TITLE: RECOMBINATION AND MUTAGENESIS IN RAD-6 MUTANTS OF SACCHAROMYCES-CEREVISIAE EVIDENCE FOR MULTIPLE FUNCTIONS OF THE RAD-6 GENE.
AUTHOR(S): MONTELONE B A [Reprint author]; PRAKASH S; PRAKASH L
CORPORATE SOURCE: DEP OF RADIATION BIOLOGY AND BIOPHYSICS, SCH OF MED, UNIV OF ROCHESTER, ROCHESTER, NY 14642, USA
SOURCE: Molecular and General Genetics, (1981) Vol. 184, No. 3, pp. 410-415.
CODEN: MGGEAE. ISSN: 0026-8925.

DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH

L5 ANSWER 5 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
TI SIMPLE MENDELIAN INHERITANCE OF THE **REITERATED RIBOSOMAL DNA** OF YEAST.
AB A diploid strain of yeast (Saccharomyces cerevisiae) was heterozygous for 2 forms of the highly repetitious ribosomal DNA. These forms could be distinguished by the pattern of fragments produced after digestion with the site-specific restriction endonuclease EcoRI. The mode of inheritance of ribosomal DNA was determined by tetrad analysis. Of 14 tetrads analyzed, 12 clearly showed the ribosomal DNA forms segregating as a single Mendelian unit. The simplest interpretation of this result is that all of the approximately 100 copies of the ribosomal DNA genes of the yeast cell are located on 1 chromosome and that meiotic recombination within these genes is suppressed. Two of the 14 tetrads showed the segregation patterns expected as the result of mitotic recombination within the ribosomal DNA. [The DNA probe was prepared from an Escherichia coli strain].
ACCESSION NUMBER: 1978:158913 BIOSIS
DOCUMENT NUMBER: PREV197865045913; BA65:45913
TITLE: SIMPLE MENDELIAN INHERITANCE OF THE **REITERATED RIBOSOMAL DNA** OF YEAST.
AUTHOR(S): PETES T D [Reprint author]; BOTSTEIN D
CORPORATE SOURCE: DEP MICROBIOL, 920 E 58TH ST, UNIV CHIC, CHICAGO, ILL 60637, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1977) Vol. 74, No. 11, pp. 5091-5095.
CODEN: PNASA6. ISSN: 0027-8424.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH

L5 ANSWER 6 OF 13 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
AN AAV12824 DNA DGENE
AB This sequence represents an amplification primer for the yeast 5S rDNA sequence. The amplified sequence can be used in the yeast of the invention, which ferments xylose to ethanol. The yeast comprises: (a) xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK) genes integrated at each of its multiple **reiterated ribosomal DNA** sites; (b) multiple copies of exogenous DNA, including XR, XD, and XK genes, fused to non-glucose inhibited promoters integrated into its chromosomal DNA, where the yeast simultaneously ferments glucose and xylose to ethanol; or (c) multiple copies of an introduced DNA containing XR, XD and XK genes, where the yeast ferments xylose to ethanol; the yeasts of (b) and (c) retain their capacity for fermenting xylose to ethanol when cultured under non-selective conditions for at least 20 generations. The yeast is produced by integrating multiple copies of exogenous DNA into reiterated chromosomal DNA of cells. The yeast produced by the integration method, even upon culture in non-selective medium for multiple generations (e.g. up to 20), retain their full capability to ferment xylose to ethanol.
ACCESSION NUMBER: AAV12824 DNA DGENE
TITLE: Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
INVENTOR: Chen Z; Ho N W Y
PATENT ASSIGNEE: (PURD)PURDUE RES FOUND.

PATENT INFO: WO 9742307 A1 19971113 66p
APPLICATION INFO: WO 1997-US7663 19970506
PRIORITY INFO: US 1996-16865 19960506
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1997-558974 [51]
DESCRIPTION: Primer for yeast 5S rDNA sequence.

L5 ANSWER 7 OF 13 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
AN AAV12829 DNA DGENE
AB This sequence is an amplification primer for the yeast Tn903 kanamycin resistance gene. The amplified sequence can be used in the yeast of the invention, which ferments xylose to ethanol. The yeast comprises: (a) xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK) genes integrated at each of its multiple **reiterated ribosomal DNA** sites; (b) multiple copies of exogenous DNA, including XR, XD, and XK genes, fused to non-glucose inhibited promoters integrated into its chromosomal DNA, where the yeast simultaneously ferments glucose and xylose to ethanol; or (c) multiple copies of an introduced DNA containing XR, XD and XK genes, where the yeast ferments xylose to ethanol; the yeasts of (b) and (c) retain their capacity for fermenting xylose to ethanol when cultured under non-selective conditions for at least 20 generations. The yeast is produced by integrating multiple copies of exogenous DNA into reiterated chromosomal DNA of cells. The yeast produced by the integration method, even upon culture in non-selective medium for multiple generations (e.g. up to 20), retain their full capability to ferment xylose to ethanol.
ACCESSION NUMBER: AAV12829 DNA DGENE
TITLE: Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
INVENTOR: Chen Z; Ho N W Y
PATENT ASSIGNEE: (PURD) PURDUE RES FOUND.
PATENT INFO: WO 9742307 A1 19971113 66p
APPLICATION INFO: WO 1997-US7663 19970506
PRIORITY INFO: US 1996-16865 19960506
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1997-558974 [51]
DESCRIPTION: Primer for yeast Tn 903 kanamycin resistance gene.

L5 ANSWER 8 OF 13 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
AN AAV12828 DNA DGENE
AB This sequence is an amplification primer for the yeast Tn903 kanamycin resistance gene. The amplified sequence can be used in the yeast of the invention, which ferments xylose to ethanol. The yeast comprises: (a) xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK) genes integrated at each of its multiple **reiterated ribosomal DNA** sites; (b) multiple copies of exogenous DNA, including XR, XD, and XK genes, fused to non-glucose inhibited promoters integrated into its chromosomal DNA, where the yeast simultaneously ferments glucose and xylose to ethanol; or (c) multiple copies of an introduced DNA containing XR, XD and XK genes, where the yeast ferments xylose to ethanol; the yeasts of (b) and (c) retain their capacity for fermenting xylose to ethanol when cultured under non-selective conditions for at least 20 generations. The yeast is produced by integrating multiple copies of exogenous DNA into reiterated

chromosomal DNA of cells. The yeast produced by the integration method, even upon culture in non-selective medium for multiple generations (e.g. up to 20), retain their full capability to ferment xylose to ethanol.

ACCESSION NUMBER: AAV12828 DNA DGENE
TITLE: Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
INVENTOR: Chen Z; Ho N W Y
PATENT ASSIGNEE: (PURD) PURDUE RES FOUND.
PATENT INFO: WO 9742307 A1 19971113 66p
APPLICATION INFO: WO 1997-US7663 19970506
PRIORITY INFO: US 1996-16865 19960506
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1997-558974 [51]
DESCRIPTION: Primer for yeast Tn 903 kanamycin resistance gene.

L5 ANSWER 9 OF 13 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
AN AAV12827 DNA DGENE
AB This sequence is an amplification primer for the yeast Tn903 kanamycin resistance gene. The amplified sequence can be used in the yeast of the invention, which ferments xylose to ethanol. The yeast comprises: (a) xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK) genes integrated at each of its multiple **reiterated ribosomal DNA** sites; (b) multiple copies of exogenous DNA, including XR, XD, and XK genes, fused to non-glucose inhibited promoters integrated into its chromosomal DNA, where the yeast simultaneously ferments glucose and xylose to ethanol; or (c) multiple copies of an introduced DNA containing XR, XD and XK genes, where the yeast ferments xylose to ethanol; the yeasts of (b) and (c) retain their capacity for fermenting xylose to ethanol when cultured under non-selective conditions for at least 20 generations. The yeast is produced by integrating multiple copies of exogenous DNA into reiterated chromosomal DNA of cells. The yeast produced by the integration method, even upon culture in non-selective medium for multiple generations (e.g. up to 20), retain their full capability to ferment xylose to ethanol.

ACCESSION NUMBER: AAV12827 DNA DGENE
TITLE: Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
INVENTOR: Chen Z; Ho N W Y
PATENT ASSIGNEE: (PURD) PURDUE RES FOUND.
PATENT INFO: WO 9742307 A1 19971113 66p
APPLICATION INFO: WO 1997-US7663 19970506
PRIORITY INFO: US 1996-16865 19960506
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1997-558974 [51]
DESCRIPTION: Primer for yeast Tn 903 kanamycin resistance gene.

L5 ANSWER 10 OF 13 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
AN AAV12826 DNA DGENE
AB This sequence is an amplification primer for the yeast Tn903 kanamycin resistance gene. The amplified sequence can be used in the yeast of the invention, which ferments xylose to ethanol. The yeast comprises: (a) xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK)

genes integrated at each of its multiple **reiterated ribosomal DNA** sites; (b) multiple copies of exogenous DNA, including XR, XD, and XK genes, fused to non-glucose inhibited promoters integrated into its chromosomal DNA, where the yeast simultaneously ferments glucose and xylose to ethanol; or (c) multiple copies of an introduced DNA containing XR, XD and XK genes, where the yeast ferments xylose to ethanol; the yeasts of (b) and (c) retain their capacity for fermenting xylose to ethanol when cultured under non-selective conditions for at least 20 generations. The yeast is produced by integrating multiple copies of exogenous DNA into reiterated chromosomal DNA of cells. The yeast produced by the integration method, even upon culture in non-selective medium for multiple generations (e.g. up to 20), retain their full capability to ferment xylose to ethanol.

ACCESSION NUMBER: AAV12826 DNA DGENE
TITLE: Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
INVENTOR: Chen Z; Ho N W Y
PATENT ASSIGNEE: (PURD) PURDUE RES FOUND.
PATENT INFO: WO 9742307 A1 19971113 66p
APPLICATION INFO: WO 1997-US7663 19970506
PRIORITY INFO: US 1996-16865 19960506
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1997-558974 [51]
DESCRIPTION: Primer for yeast Tn 903 kanamycin resistance gene.

L5 ANSWER 11 OF 13 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN
TI Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
AN AAV12825 DNA DGENE
AB This sequence represents an amplification primer for the yeast 5S rDNA sequence. The amplified sequence can be used in the yeast of the invention, which ferments xylose to ethanol. The yeast comprises: (a) xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK) genes integrated at each of its multiple **reiterated ribosomal DNA** sites; (b) multiple copies of exogenous DNA, including XR, XD, and XK genes, fused to non-glucose inhibited promoters integrated into its chromosomal DNA, where the yeast simultaneously ferments glucose and xylose to ethanol; or (c) multiple copies of an introduced DNA containing XR, XD and XK genes, where the yeast ferments xylose to ethanol; the yeasts of (b) and (c) retain their capacity for fermenting xylose to ethanol when cultured under non-selective conditions for at least 20 generations. The yeast is produced by integrating multiple copies of exogenous DNA into reiterated chromosomal DNA of cells. The yeast produced by the integration method, even upon culture in non-selective medium for multiple generations (e.g. up to 20), retain their full capability to ferment xylose to ethanol.

ACCESSION NUMBER: AAV12825 DNA DGENE
TITLE: Yeast which ferments xylose to methanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites
INVENTOR: Chen Z; Ho N W Y
PATENT ASSIGNEE: (PURD) PURDUE RES FOUND.
PATENT INFO: WO 9742307 A1 19971113 66p
APPLICATION INFO: WO 1997-US7663 19970506
PRIORITY INFO: US 1996-16865 19960506
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 1997-558974 [51]
DESCRIPTION: Primer for yeast 5S rDNA sequence.

L5 ANSWER 12 OF 13 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
TI Simple Mendelian inheritance of the **reiterated ribosomal DNA** of yeast.
ACCESSION NUMBER: 78243218 EMBASE
DOCUMENT NUMBER: 1978243218
TITLE: Simple Mendelian inheritance of the **reiterated ribosomal DNA** of yeast.
AUTHOR: Petes T.D.; Botstein D.
CORPORATE SOURCE: Dept. Biol., MIT, Cambridge, Mass. 02139, United States
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1977) 74/11 (5091-5095). CODEN: PNASA6
COUNTRY: United States
DOCUMENT TYPE: Journal
FILE SEGMENT: 022 Human Genetics
LANGUAGE: English

L5 ANSWER 13 OF 13 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
TI Yeast which ferments xylose to ethanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites.
AN 1997-558974 [51] WPIDS
AB WO 9742307 A UPAB: 19991020
Novel yeast which ferments xylose to ethanol, comprises: (a) xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK) genes integrated at each of its multiple **reiterated ribosomal DNA** sites; (b) multiple copies of exogenous DNA, including XR, XD, and XK genes, fused to non-glucose inhibited promoters integrated into its chromosomal DNA, where the yeast simultaneously ferments glucose and xylose to ethanol; or (c) multiple copies of an introduced DNA containing XR, XD and XK genes, where the yeast ferments xylose to ethanol, where the yeasts of (b) and (c) retain their capacity for fermenting xylose to ethanol when cultured under non-selective conditions for at least 20 generations.
USE - The methods can produce yeast, which even upon culture in non-selective medium for multiple generations, e.g. up to 20, retain their full capability to ferment xylose to ethanol.
Dwg.0/12
ACCESSION NUMBER: 1997-558974 [51] WPIDS
DOC. NO. CPI: C1997-178545
TITLE: Yeast which ferments xylose to ethanol - comprising xylitol reductase, xylitol dehydrogenase and xylulokinase genes integrated at each of its multiple **reiterated ribosomal DNA** sites.
DERWENT CLASS: D16 D17 E17 H06
INVENTOR(S): CHEN, Z; HO, N W Y
PATENT ASSIGNEE(S): (PURD) PURDUE RES FOUND
COUNTRY COUNT: 76
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9742307	A1	19971113	(199751)*	EN	66
RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN YU					
AU 9728301	A	19971126	(199813)		
EP 898616	A1	19990303	(199913)	EN	
R: AT BE DE DK ES FI FR GB GR IE IT NL PT SE					

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     CN 1225125     A  19990804 (199949)
     JP 2000509988 W   20000808 (200043)        50
     MX 9809223     A1 19990701 (200061)
     AU 731102      B  20010322 (200122)
     BR 9710963     A  20010731 (200146)

APPLICATION DETAILS:

     PATENT NO    KIND                    APPLICATION       DATE
     ------------------------------------------------------------
     WO 9742307     A1                    WO 1997-US7663    19970506
     AU 9728301     A                     AU 1997-28301     19970506
     EP 898616      A1                    EP 1997-922698    19970506
                                          WO 1997-US7663    19970506
     CN 1225125     A                     CN 1997-196195    19970506
     JP 2000509988 W                      JP 1997-540153    19970506
                                          WO 1997-US7663    19970506
     MX 9809223     A1                    MX 1998-9223      19981105
     AU 731102      B                     AU 1997-28301     19970506
     BR 9710963     A                     BR 1997-10963     19970506
                                          WO 1997-US7663    19970506

FILING DETAILS:

     PATENT NO    KIND                    PATENT NO
     ------------------------------------------------
     AU 9728301     A  Based on           WO 9742307
     EP 898616      A1 Based on           WO 9742307
     JP 2000509988 W   Based on           WO 9742307
     AU 731102      B  Previous Publ.     AU 9728301
                       Based on           WO 9742307
     BR 9710963     A  Based on           WO 9742307

PRIORITY APPLN. INFO: US 1996-16865P    19960506


=> d his

     (FILE 'HOME' ENTERED AT 17:37:06 ON 10 FEB 2004)

     FILE 'MEDLINE, BIOSIS, USPATFULL, DGENE, EMBASE, WPIDS, FSTA, JAPIO,
     JICST-EPLUS' ENTERED AT 17:37:27 ON 10 FEB 2004
L1             6 S GENE () REITERATED
L2         19510 S RIBOSOMAL DNA
L3             6 S L1 AND L1
L4             0 S L1 AND L2
L5            13 S REITERATED RIBOSOMAL DNA
L6          1278 S GENE INTEGRATED

=> s l6 and l5
L7             0 L6 AND L5

=> s gene integrated () reiterated ribosomal DNA
L8             0 GENE INTEGRATED (W) REITERATED RIBOSOMAL DNA

=> s integrated gene and reiterated ribosomal DNA
L9             0 INTEGRATED GENE AND REITERATED RIBOSOMAL DNA

=> s l6 and l2
L10           11 L6 AND L2

=> d l10 ti abs ibib tot

L10  ANSWER 1 OF 11     MEDLINE on STN
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TI High-copy-number integration into the **ribosomal DNA** of Saccharomyces cerevisiae: a new vector for high-level expression.

AB Yeast vectors suitable for high-level expression of heterologous proteins should combine a high copy number with a high mitotic stability under non-selective conditions. Since high stability can best be assured by integration of the vector into chromosomal DNA we have set out to design a vector that is able to integrate into the yeast genome in a large number of copies. The rDNA locus appeared to be an attractive target for such multiple integration since it encompasses 100-200 tandemly repeated units. Plasmids containing several kb of rDNA for targeted homologous recombination, as well as the deficient LEU2-d selection marker were constructed and, after transformation into yeast, tested for both copy number and stability. One of these plasmids, designated pMIRY2 (for multiple integration into **ribosomal DNA** in yeast), was found to be present in 100-200 copies per cell by restriction analysis. The pMIRY2 transformants retained 80-100% of the plasmid copies over a period of 70 generations of growth in batch culture under non-selective conditions. To explore the potential of pMIRY2 as an expression vector we have inserted the homologous genes for phosphoglycerate kinase (PGK) and Mn2+-dependent superoxide dismutase (SOD) as well as the heterologous genes for thaumatin from Thaumatococcus danielli (under the GAPDH promoter), into this plasmid and analyzed the yield of the various proteins. Under optimized conditions the level of PGK in cells transformed with pMIRY2-PGK was about 50% of total soluble protein. The yield of thaumatin in the pMIRY2-thaumatin transformants exceeded by about a factor of 100 the level of thaumatin observed in transformants carrying only a single thaumatin **gene integrated** at the TRP1 locus in chromosome IV.

ACCESSION NUMBER: 90006749 MEDLINE
DOCUMENT NUMBER: 90006749 PubMed ID: 2676725
TITLE: High-copy-number integration into the **ribosomal DNA** of Saccharomyces cerevisiae: a new vector for high-level expression.
AUTHOR: Lopes T S; Klootwijk J; Veenstra A E; van der Aar P C; van Heerikhuizen H; Raue H A; Planta R J
CORPORATE SOURCE: Biochemisch Laboratorium, Vrije Universiteit, Amsterdam, The Netherlands.
SOURCE: GENE, (1989 Jul 15) 79 (2) 199-206.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198911
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19900328
Entered Medline: 19891108

L10 ANSWER 2 OF 11 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

TI HIGH-COPY-NUMBER INTEGRATION INTO THE **RIBOSOMAL DNA** OF SACCHAROMYCES-CEREVISIAE A NEW VECTOR FOR HIGH-LEVEL EXPRESSION.

AB Yeast vectors suitable for high-level expression of heterologous proteins should combine a high copy number with a high mitotic stability under non-selective conditions. Since high stability can best be assured by integration of the vector into chromosomal DNA we have set out to design a vector that is able to integrate into the yeast genome in a large number of copies. The rDNA locus appeared to be an attractive target for such multiple integration since it encompasses 100-200 tandemly repeated units. Plasmid containing several kb of rDNA for targeted homologous recombination, as well as the deficient LEU2-d selection marker were constructed and, after transformation into yeast, tested for both copy number and stability. One of these plasmids, designated pMIRY2 (for multiple integration into **ribosomal DNA** in yeast), was found to be present in 100-200 copies per cell by restriction analysis.

The pMIRY2 transformants retained 80-100% of the plasmid copies over a period of 70 generations of growth in batch culture under non-selective conditions. To explore the potential of pMIRY2 as an expression vector we have inserted the homologous genes for phosphoglycerate kinase (PGK) and Mn2+-dependent superoxide dismutase (SOD) as well as the heterologous genes for thaumatin from Thaumatococcus danielli (under the GAPDH promoter), into this plasmid and analyzed the yield of the various proteins. Under optimized conditions the level of PGK in cells transformed with pMIRY2-PGK was about 50% of total soluble protein. The yield of thaumatin in the pMIRY2-thaumatin transformants exceeded by about a factor of 100 the level of thaumatin observed in transformants carrying only a single thaumatin **gene integrated** at the TRP1 locus in chromosome IV.

ACCESSION NUMBER: 1989:426983 BIOSIS
DOCUMENT NUMBER: PREV198988085241; BA88:85241
TITLE: HIGH-COPY-NUMBER INTEGRATION INTO THE **RIBOSOMAL DNA** OF SACCHAROMYCES-CEREVISIAE A NEW VECTOR FOR HIGH-LEVEL EXPRESSION.
AUTHOR(S): LOPES T S [Reprint author]; KLOOTWIJK J; VEENSTRA A E; VAN DER AAR P C; VAN HEERIKHUIZEN H; RAUE H A; PLANTA R J
CORPORATE SOURCE: BIOCHEM LAB, VRIJE UNIV, DE BOELELAAN 1083, 1081 HV AMSTERDAM, NETHLAB
SOURCE: Gene (Amsterdam), (1989) Vol. 79, No. 2, pp. 199-206. CODEN: GENED6. ISSN: 0378-1119.
DOCUMENT TYPE: Article
FILE SEGMENT: BA
LANGUAGE: ENGLISH
ENTRY DATE: Entered STN: 19 Sep 1989
Last Updated on STN: 19 Sep 1989

L10 ANSWER 3 OF 11 USPATFULL on STN
TI Transgenic plants
AB The invention provides method for producing a transgenic plant comprising a recombinant plastid genome containing an exogenous gene in the absence of a selectable marker gene introduced with the exogenous gene by using direct repeat sequences, nucleic acid constructs containing direct repeat sequences which may be used in the method and transgenic plants produced by the method.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2003:267318 USPATFULL
TITLE: Transgenic plants
INVENTOR(S): Day, Anil, Cheshire, UNITED KINGDOM
Iamtham, Siriluck, Nontaburee, THAILAND
Zubko, Mikhajo, Cheshire, UNITED KINGDOM

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003188337	A1	20031002	
APPLICATION INFO.:	US 2003-258253	A1	20030325	(10)
	WO 2001-GB1761		20010420	

	NUMBER	DATE
PRIORITY INFORMATION:	GB 2000-9780	20000420
	GB 2000-9968	20000425
	GB 2000-17338	20000715

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Joshua R Slavitt, Synnestvedt & Lechner, 1101 Market Street, 2600 Aramark Tower, Philadelphia, PA, 19107-2950
NUMBER OF CLAIMS: 61
EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS: 13 Drawing Page(s)
LINE COUNT: 1610
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 4 OF 11 USPATFULL on STN
TI Yeast vector and method of producing proteins using the same
AB An object of the present invention is to provide a vector which can be integrated into a yeast chromosome in a high number of copies. Another object of the present invention is to provide a modified vector which can be integrated into the yeast chromosome in a high number of copies and of which expression units stably maintain on the chromosome. The vector according to the present invention comprises a marker gene for selecting transformants, a shortened promoter sequence which is operably linked to the marker gene and a sequence homologous to the chromosomal DNA of Candida utilis, and optionally a heterologous gene or a gene derived from C. utilis, wherein the vector is linearized by cleaving within said homologous DNA sequence or at both ends of the homologous DNA sequence with restriction enzymes, and wherein the heterologous gene or the gene derived from C. utilis can be integrated into the chromosomal DNA of C. utilis by homologous recombination.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:213840 USPATFULL
TITLE: Yeast vector and method of producing proteins using the same
INVENTOR(S): Kondo, Keiji, Yokohama-shi, JAPAN
Miura, Yutaka, Yokohama-shi, JAPAN

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002115220	A1	20020822
	US 6610514	B2	20030826
APPLICATION INFO.:	US 2001-908855	A1	20010720 (9)

RELATED APPLN. INFO.: Division of Ser. No. US 1999-242690, filed on 23 Feb 1999, PATENTED A 371 of International Ser. No. WO 1997-JP2924, filed on 22 Aug 1997, UNKNOWN

	NUMBER	DATE
PRIORITY INFORMATION:	JP 1996-241062	19960823

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Stephen A. Bent, FOLEY & LARDNER, Washington Harbour, 3000 K Street, NW., Suite 500, Washington, DC, 20007-5109
NUMBER OF CLAIMS: 61
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 29 Drawing Page(s)
LINE COUNT: 2623
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 5 OF 11 USPATFULL on STN
TI Transposition assembly for gene transfer in eukaryotes
AB A transposition assembly for the transfer of a DNA fragment of interest into the ribosomal nuclear DNA of an eukaryotic cell. An insertion means, an eukaryotic cell and a pharmaceutical composition comprising said transposition assembly, as well as a method for the in vitro transfer of said DNA fragment, are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2002:29276 USPATFULL
TITLE: Transposition assembly for gene transfer in eukaryotes
INVENTOR(S): Jacobs, Eric, Dorlisheim, FRANCE
PATENT ASSIGNEE(S): Transgene S.A., Strasbourg, FRANCE (non-U.S.

corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6346414	B1	20020212	
	WO 9424300		19941027	
APPLICATION INFO.:	US 1995-532657		19951016	(8)
	WO 1994-FR419		19940414	
			19951016	PCT 371 date

	NUMBER	DATE
PRIORITY INFORMATION:	FR 1993-4530	19930416

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Priebe, Scott D.
LEGAL REPRESENTATIVE: Burns, Doane, Swecker & Mathis, L.L.P.
NUMBER OF CLAIMS: 12
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 1 Drawing Figure(s); 1 Drawing Page(s)
LINE COUNT: 889
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 6 OF 11 USPATFULL on STN
TI Yeast vector comprising a shortened promoter sequence
AB An object of the present invention is to provide a vector which can be integrated into a yeast chromosome in a high number of copies. Another object of the present invention is to provide a modified vector which can be integrated into the yeast chromosome in a high number of copies and of which expression units stably maintain on the chromosome. The vector according to the present invention comprises a marker gene for selecting transformants, a shortened promoter sequence which is operably linked to the marker gene and a sequence homologous to the chromosomal DNA of Candida utilis, and optionally a heterologous gene or a gene derived from C. utilis, wherein the vector is linearized by cleaving within said homologous DNA sequence or at both ends of the homologous DNA sequence with restriction enzymes, and wherein the heterologous gene or the gene derived from C. utilis can be integrated into the chromosomal DNA of C. utilis by homologous recombination.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2001:147745 USPATFULL
TITLE: Yeast vector comprising a shortened promoter sequence
INVENTOR(S): Kondo, Keiji, Yokohama, Japan
Miura, Yutaka, Yokohama, Japan
PATENT ASSIGNEE(S): Kirin Beer Kabushiki Kaisha, Tokyo, Japan (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6284534	B1	20010904	
	WO 9807873		19980226	
APPLICATION INFO.:	US 1999-242690		19990223	(9)
	WO 1997-JP2924		19970822	
			19990223	PCT 371 date
			19990223	PCT 102(e) date

	NUMBER	DATE
PRIORITY INFORMATION:	JP 1996-241062	19960823

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: McKelvey, Terry
LEGAL REPRESENTATIVE: Foley & Lardner

NUMBER OF CLAIMS: 16
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 29 Drawing Figure(s); 29 Drawing Page(s)
LINE COUNT: 1749
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 7 OF 11 USPATFULL on STN
TI Yeast cells comprising at least two copies of a desired **gene integrated** into the chromosomal genome at more than one non-ribosomal RNA encoding domain, particularly with Kluyveromyces
AB The present invention provides for a yeast cell comprising at least two copies of a desired **gene integrated** into its chromosomal genome, wherein said genome comprises at least two DNA domains suitable for integration of one or more copies of said desired gene, which domains share substantial sequence homology and are non-ribosomal RNA encoding DNA domains, and wherein at least two of said substantially homologous non-ribosomal RNA encoding DNA domains have at least one copy of the said desired **gene integrated**. The invention also provides methods for making yeast cells according to the invention, as well as the use thereof for making a protein, a peptide or a metabolite.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 2001:116792 USPATFULL
TITLE: Yeast cells comprising at least two copies of a desired **gene integrated** into the chromosomal genome at more than one non-ribosomal RNA encoding domain, particularly with Kluyveromyces
INVENTOR(S): Swinkels, Bart Willem, Delft, Netherlands
Van Ooijen, Albert Johannes Joseph, Voorburg, Netherlands
Noordermeer-Van Der Haak, Adriana Cornelia Maria, Wateringen, Netherlands
PATENT ASSIGNEE(S): DSM N.V., Te Heerlen, Netherlands (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6265186	B1	20010724	
	WO 9846774		19981022	
APPLICATION INFO.:	US 1999-402817		19991210	(9)
	WO 1998-EP2261		19980414	
			19991210	PCT 371 date
			19991210	PCT 102(e) date

	NUMBER	DATE
PRIORITY INFORMATION:	EP 1997-201053	19970411

DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Schwartzman, Robert A.
ASSISTANT EXAMINER: Davis, Katharine F
LEGAL REPRESENTATIVE: McDonnell Boehnen Hulbert & Berghoff
NUMBER OF CLAIMS: 45
EXEMPLARY CLAIM: 18
NUMBER OF DRAWINGS: 11 Drawing Figure(s); 11 Drawing Page(s)
LINE COUNT: 1658
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 8 OF 11 USPATFULL on STN
TI Yeast silencing genes proteins and methods
AB The present invention provides the yeast genes SAS2, SAS3 and ESA1 and the proteins encoded thereby. SAS2, SAS3 and ESA1 genes of members of the genus Saccharomyces are provided, particularly the SAS2, SAS3 and

ESA1 genes of S. cerevisiae. Also provided are yeast SAS2, SAS3 and ESA1 coding sequences. Specifically provided are the SAS2, SAS3 and ESA1 coding sequences of members of the genus Saccharomyces, and more specifically of S. cerevisiae. Genes of this invention comprise protein coding sequences as well as the regulatory regions that control expression of the encoded protein. Of most interest are SAS2, SAS3, and ESA1 genes of yeast including those of the genus Saccharomyces which are 90% or more homologous to the corresponding genes of S. cerevisiae. Specifically provided are DNA constructs comprising purified and isolated DNA molecules comprising SAS2, SAS3 or ESA1 coding sequences that encode proteins from a strain of S. cerevisiae.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1999:151000 USPATFULL
TITLE:	Yeast silencing genes proteins and methods
INVENTOR(S):	Pillus, Lorraine, Boulder, CO, United States Clarke, Astrid, Longmont, CO, United States Lowell, Joanna, Boulder, CO, United States Jacobson, Sandra, Lafayette, CO, United States Reifsnyder, Cheryl, Boulder, CO, United States
PATENT ASSIGNEE(S):	University Technology Corporation, Boulder, CO, United States (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 5989897		19991123	
APPLICATION INFO.:	US 1998-47026		19980324	(9)

	NUMBER	DATE	
PRIORITY INFORMATION:	US 1997-42375P	19970324	(60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	Granted
PRIMARY EXAMINER:	McKelvey, Terry
LEGAL REPRESENTATIVE:	Greenlee, Winner and Sullivan, PC
NUMBER OF CLAIMS:	8
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	6 Drawing Figure(s); 6 Drawing Page(s)
LINE COUNT:	2476

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 9 OF 11 USPATFULL on STN

TI Transformation systems for the yeast candida utilis and the expression of heterologous genes therewith

AB An reproducible transformation system of a yeast of Candida utilis, a process for expressing a heterologous gene in the transformation system, a vector which can be used in the transformation system and the expression method, and a novel DNA group are disclosed. In particular, the process for expressing a heterologous gene in Candida utilis comprises transforming Candida utilis with a vector comprising a drug-resistance marker, a sequence homologous to the chromosomal DNA of the Candida utilis yeast, and the heterologous gene, culturing the transformant, and isolating the expression product of the heterologous gene.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:	1998:157136 USPATFULL
TITLE:	Transformation systems for the yeast candida utilis and the expression of heterologous genes therewith
INVENTOR(S):	Kondo, Keiji, Yokohama, Japan Kajiwara, Susumu, Tokyo-to, Japan Misawa, Norihiko, Yokohama, Japan
PATENT ASSIGNEE(S):	Kirin Beer Kabushiki Kaisha, Tokyo, Japan (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 5849524		19981215	
	WO 9532289		19951130	
APPLICATION INFO.:	US 1996-557128		19960524	(8)
	WO 1995-JP1005		19950525	
			19960524	PCT 371 date
			19960524	PCT 102(e) date

	NUMBER	DATE
PRIORITY INFORMATION:	JP 1994-135015	19940525
	JP 1994-285823	19941026
	JP 1995-129287	19950428

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Ketter, James
ASSISTANT EXAMINER: Yucel, Irem
LEGAL REPRESENTATIVE: Foley & Lardner
NUMBER OF CLAIMS: 101
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 51 Drawing Figure(s); 50 Drawing Page(s)
LINE COUNT: 4096
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 10 OF 11 USPATFULL on STN
TI Process for the genetic modification of yeast
AB Yeast is genetically modified by transformation with an integration vector comprising two copies of a homologous 2 μm plasmid DNA sequence in direct orientation relative to one another and encompassing the said DNA sequence, and then isolating, from the transformed yeast obtained, cells containing the endogenous 2 μm plasmid modified by incorporation of the said DNA sequence but not containing the said vector. The resulting yeast can be maintained under non-selective growth conditions.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
ACCESSION NUMBER: 90:50747 USPATFULL
TITLE: Process for the genetic modification of yeast
INVENTOR(S): Hinchliffe, Edward, Burton Joyce, England
Fleming, Christine J., Leicestershire, England
PATENT ASSIGNEE(S): Delta Biotechnology Limited, Burton-on-Trent, England (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 4937193		19900626	
APPLICATION INFO.:	US 1987-66931		19870626	(7)

	NUMBER	DATE
PRIORITY INFORMATION:	GB 1986-15701	19860627

DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Teskin, Robin
LEGAL REPRESENTATIVE: Cushman, Darby & Cushman
NUMBER OF CLAIMS: 14
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)
LINE COUNT: 524
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 11 OF 11 EMBASE

on STN

TI High-copy-number integration into the **ribosomal DNA** of Saccharomyces cerevisiae: A new vector for high-level expression.

AB Yeast vectors suitable for high-level expression of heterologous proteins should combine a high copy number with a high mitotic stability under non-selective conditions. Since high stability can best be assured by integration of the vector into chromosomal DNA we have set out to design a vector that is able to integrate into the yeast genome in a large number of copies. The rDNA locus appeared to be an attractive target for such multiple integration since it encompasses 100-200 tandemly repeated units. Plasmids containing several kb of rDNA for targeted homologous recombination, as wel as the deficient LEU2-d selection marker were constructed and, after transformation into yeast, tested for both copy number and stability. One of these plasmids, designated pMIRY2 (for multiple integration into **ribosomal DNA** in yeast), was found to be prseent in 100-200 copies per cell by restriction analysis. The pMIRY2 transformants retained 80-100% of the plasmid copies over a period of 70 generations of growth in batch culture under non-selective conditions. To explore the potential of pMIRY2 as an expression vector we have inserted the homologous genes for phosphoglycerate kinase (PGK) and Mn2+-dependent superoxide dismutase (SOD) as well as the heterologous genes for thaumatin from Thaumatococcus danielli (under the GAPDH promoter), into this plasmid and analyzed the yield of the various proteins. Under optimized conditions the level of PGK in cells transformed with pMIRY2-PGK was about 50% of total soluble protein. The yield of thaumatin in the pMIRY2-thaumatin transformants exceeded by about a factor of 100 the level of thaumatin observed in transformants carrying only a single thaumatin **gene integrated** at the TRP1 locus in chromosome IV.

ACCESSION NUMBER: 89183241 EMBASE
DOCUMENT NUMBER: 1989183241

TITLE: High-copy-number integration into the **ribosomal DNA** of Saccharomyces cerevisiae: A new vector for high-level expression.

AUTHOR: Lopes T.S.; Klootwijk J.; Veenstra A.E.; Van der Aar P.C.; Van Heerikhuizen H.; Raue H.A.; Planta R.J.
CORPORATE SOURCE: Microbiologisch Laboratorium, Vrije Universiteit, 1081 HV Amsterdam, Netherlands

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